



SEQUENCE LISTING

45
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<110> Zhou, Ming-Ming
<120> Methods of Identifying Modulators of the FGF Receptor
<130> 2459-1-002N
<140> 09/757415
<141> 2001-01-09
<150> 60/175867
<151> 2000-01-12
<160> 7
<170> PatentIn version 3.1
<210> 1
<211> 508
<212> PRT
<213> Homo sapien
<400> 1
Met Gly Ser Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn
1 5 10 15
His Arg Asn Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu
20 25 30
Leu Gly Ser Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr
35 40 45
Thr Arg Lys Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg
50 55 60
Tyr Gly Tyr Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Arg Arg Cys
65 70 75 80
Gln Thr Gly Gln Gly Ile Phe Ala Phe Lys Cys Ala Arg Ala Glu Glu
85 90 95
Leu Phe Asn Met Leu Gln Glu Ile Met Gln Asn Asn Ser Ile Asn Val
100 105 110
Val Glu Glu Pro Val Val Glu Arg Asn Asn His Gln Thr Glu Leu Glu
115 120 125
Val Pro Arg Thr Pro Arg Thr Pro Thr Thr Pro Gly Phe Ala Ala Gln
130 135 140

Asn Leu Pro Asn Gly Tyr Pro Arg Tyr Pro Ser Phe Gly Asp Ala Ser
 145 150 155 160

Ser His Pro Ser Ser Arg His Pro Ser Val Gly Ser Ala Arg Leu Pro
 165 170 175

Ser Val Gly Glu Glu Ser Thr His Pro Leu Leu Val Ala Glu Glu Gln
 180 185 190

Val His Thr Tyr Val Asn Thr Thr Gly Val Gln Glu Glu Arg Lys Asn
 195 200 205

Arg Thr Ser Val His Val Pro Leu Glu Ala Arg Val Ser Asn Ala Glu
 210 215 220

Ser Ser Thr Pro Lys Glu Glu Pro Ser Ser Ile Glu Asp Arg Asp Pro
 225 230 235 240

Gln Ile Leu Leu Glu Pro Glu Gly Val Lys Phe Val Leu Gly Pro Thr
 245 250 255

Pro Val Gln Lys Gln Leu Met Glu Lys Glu Lys Leu Glu Gln Leu Gly
 260 265 270

Arg Asp Gln Val Ser Gly Ser Gly Ala Asn Asn Thr Glu Trp Asp Thr
 275 280 285

Gly Tyr Asp Ser Asp Glu Arg Arg Asp Ala Pro Ser Val Asn Lys Leu
 290 295 300

Val Tyr Glu Asn Ile Asn Gly Leu Ser Ile Pro Ser Ala Ser Gly Val
 305 310 315 320

Arg Arg Gly Arg Leu Thr Ser Thr Ser Thr Ser Asp Thr Gln Asn Ile
 325 330 335

Asn Asn Ser Ala Gln Arg Arg Thr Ala Leu Leu Asn Tyr Glu Asn Leu
 340 345 350

Pro Ser Leu Pro Pro Val Trp Glu Ala Arg Lys Leu Ser Arg Asp Glu
 355 360 365

Asp Asp Asn Leu Gly Pro Lys Thr Pro Ser Leu Asn Gly Tyr His Asn
 370 375 380

Asn Leu Asp Pro Met His Asn Tyr Val Asn Thr Glu Asn Val Thr Val

385 390 395 400
 Pro Ala Ser Ala His Lys Ile Glu Tyr Ser Arg Arg Arg Asp Cys Thr
 405 410 415
 Pro Thr Val Phe Asn Phe Asp Ile Arg Arg Pro Ser Leu Glu His Arg
 420 425 430
 Gln Leu Asn Tyr Ile Gln Val Asp Leu Glu Gly Gly Ser Asp Ser Asp
 435 440 445
 Asn Pro Gln Thr Pro Lys Thr Pro Thr Thr Pro Leu Pro Gln Thr Pro
 450 455 460
 Thr Arg Arg Thr Glu Leu Tyr Ala Val Ile Asp Ile Glu Arg Thr Ala
 465 470 475 480
 Ala Met Ser Asn Leu Gln Lys Ala Leu Pro Arg Asp Asp Gly Thr Ser
 485 490 495
 Arg Lys Thr Arg His Asn Ser Thr Asp Leu Pro Met
 500 505

 <210> 2
 <211> 822
 <212> PRT
 <213> Mus musculus

 <400> 2
 Met Trp Gly Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
 1 5 10 15

 Thr Leu Cys Thr Ala Arg Pro Ala Pro Thr Leu Pro Glu Gln Ala Gln
 20 25 30

 Pro Trp Gly Val Pro Val Glu Val Glu Ser Leu Leu Val His Pro Gly
 35 40 45

 Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile
 50 55 60

 Asn Trp Leu Arg Asp Gly Val Gln Leu Val Glu Ser Asn Arg Thr Arg
 65 70 75 80

 Ile Thr Gly Glu Glu Val Glu Val Arg Asp Ser Ile Pro Ala Asp Ser
 85 90 95

Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr
 100 105 110

Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp
 115 120 125

Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr
 130 135 140

Lys Pro Asn Arg Arg Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
 145 150 155 160

Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
 165 170 175

Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
 180 185 190

Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
 195 200 205

Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
 210 215 220

Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
 225 230 235 240

His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
 245 250 255

Leu Gln Ala Gly Leu Pro Ala Asn Glu Thr Val Ala Leu Gly Ser Asn
 260 265 270

Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
 275 280 285

Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
 290 295 300

Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
 305 310 315 320

Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
 325 330 335

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
 340 345 350
 Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
 355 360 365
 Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
 370 375 380
 Phe Leu Ile Ser Cys Met Leu Gly Ser Val Ile Ile Tyr Lys Met Lys
 385 390 395 400
 Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
 405 410 415
 Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
 420 425 430
 Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
 435 440 445
 Leu Ser Ser Ser Gly Thr Pro Met Pro Ala Gly Val Ser Glu Tyr Glu
 450 455 460
 Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
 465 470 475 480
 Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
 485 490 495
 Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
 500 505 510
 Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
 515 520 525
 Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
 530 535 540
 Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
 545 550 555 560
 Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
 565 570 575
 Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu

580	585	590
Glu Gln Leu Ser Ser Lys Asp	Leu Val Ser Cys Ala Tyr Gln Val Ala	
595	600	605
Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu		
610	615	620
Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala		
625	630	635 640
Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys		
645	650	655
Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu		
660	665	670
Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val		
675	680	685
Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val		
690	695	700
Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp		
705	710	715 720
Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys		
725	730	735
Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu		
740	745	750
Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Ser Gln Glu Tyr Leu Asp		
755	760	765
Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg		
770	775	780
Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro		
785	790	795 800
Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Thr Gln Leu Ala Asn		
805	810	815
Ser Gly Leu Lys Arg Arg		
820		

<210> 3
<211> 22
<212> PRT
<213> Mus musculus

<400> 3

His Ser Gln Met Ala Val His Lys Leu Ala Lys Ser Ile Pro Leu Arg
1 5 10 15

Arg Gln Val Thr Val Ser
20

<210> 4
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Tyrosine phosphorylation peptide

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is a phosphotyrosine

<400> 4

Leu Val Ile Ala Gly Asn Pro Ala Xaa Arg Ser
1 5 10

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> Xaa can be any amino acid

<220>
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<222> (5)..(7)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa can be any amino acid

<220>
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 <222> (11)..(11)
 <223> Xaa can be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (13)..(13)
 <223> Xaa can be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (15)..(15)
 <223> Xaa can be any amino acid

<400> 5

Val Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Leu Xaa Arg Xaa Val Xaa Val
 1 5 10 15

<210> 6
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Motif

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa can be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Xaa is a phosphotyrosine

<400> 6

Asn Pro Xaa Xaa
 1

<210> 7
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide derived from the TrKA receptor

<220>

<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is a phosphotyrosine

<400> 7

His Ile Ile Glu Asn Pro Gln Xaa Phe Ser Asp Ala
1 5 10